



(B)

Wed Nov 21 09:32:15 2001 [BLASTP 2.2.1 [Jul-12-2001], NCBI]
 /home/ruby/va/Molbio/carpenda/tempblast/p1.DNA59606.nc (477 aa)

BLAST RESULTS BT-1

Sequences producing High-scoring Segment Pairs:

			Score	Match	Pct	E-val
1	P_AAB65239	Human PRO1107 (UNQ550) protein sequence S	2561	477	100	0.0
2	P_AAU12397	Human PRO1107 polypeptide sequence - Homo	2561	477	100	0.0
3	P_AAY66716	Membrane-bound protein PRO1107 - Homo sap	2561	477	100	0.0
4	P_AAB24072	Human PRO1107 protein sequence SEQ ID NO:	2561	477	100	0.0
5	P_AAE05491	Human phosphodiesterase-1 (HPDE-1) - Homo	2553	475	100	0.0
6	CAB56566.1	dJ8B1.3 (similar to PLASMA-CELL MEMBRANE	2551	474	99	0.0
7	NP_067547.1	ectonucleotide pyrophosphatase/phosphodi	2551	474	99	0.0
8	A59391	probable phosphodiesterase I (EC 3.1.4.1)	2551	474	99	0.0
9	P_AAM23765	Human EST encoded protein SEQ ID NO: 1290	2403	446	99	0.0

>1 P_AAB65239 Human PRO1107 (UNQ550) protein sequence SEQ ID NO:285 - Homo (477 aa) [1 seg]

Score = 2561 (991 bits), Expect = 0.0

Identities = 477/477 (100%), Positives = 477/477 (100%), at 1,1-477,477

DNA59606.nc 1 MTSKFILVSFILAALSLSTTFSLQLDQQKVLLVSDGFRWDYLYKVPTPHYIMKYGVH

 P_AAB65239 1 MTSKFILVSFILAALSLSTTFSLQLDQQKVLLVSDGFRWDYLYKVPTPHYIMKYGVH

 DNA59606.nc 61 VKQVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRINKSFSLDHMNIYDSKFWEAA

 P_AAB65239 61 VKQVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRINKSFSLDHMNIYDSKFWEAA

 DNA59606.nc 121 TPIWITNQRAGHTSGAACWPGTDVKIHKRFPTHMPYNESVSFEDRVAKIVEWFTSKEPI

 P_AAB65239 121 TPIWITNQRAGHTSGAACWPGTDVKIHKRFPTHMPYNESVSFEDRVAKIVEWFTSKEPI

 DNA59606.nc 181 NLGLLYWEDPDDMGHHLGPDSPLMGPVISIDKKLGYLIQMLKKAKLWNTLNLIITSDHG

 P_AAB65239 181 NLGLLYWEDPDDMGHHLGPDSPLMGPVISIDKKLGYLIQMLKKAKLWNTLNLIITSDHG

 DNA59606.nc 241 MTQCSEERLIELDQYLDKDHYTLIDQSPVAAILPKEGKFDEVYEAUTHAPNLTVYKKED

 P_AAB65239 241 MTQCSEERLIELDQYLDKDHYTLIDQSPVAAILPKEGKFDEVYEAUTHAPNLTVYKKED

 DNA59606.nc 301 VPERWHYKYNNSRIQPIIAVADEGWHILQNKSDDFLLGNHGYDNALADMPIFLAHGPAFR

 P_AAB65239 301 VPERWHYKYNNSRIQPIIAVADEGWHILQNKSDDFLLGNHGYDNALADMPIFLAHGPAFR

 DNA59606.nc 361 KNFSKEAMNSTDLYPLLCHLLNITAMPHNGSFWNVQDLLNSAMPRVVPYTQSTILLPGSV

 P_AAB65239 361 KNFSKEAMNSTDLYPLLCHLLNITAMPHNGSFWNVQDLLNSAMPRVVPYTQSTILLPGSV

 DNA59606.nc 421 KPAEYDQEGSYPYFIGVSLGSIIIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA

 P_AAB65239 421 KPAEYDQEGSYPYFIGVSLGSIIIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA

>2 P_AAU12397 Human PRO1107 polypeptide sequence - Homo sapiens. (477 aa) [1 seg]

Score = 2561 (991 bits), Expect = 0.0

Identities = 477/477 (100%), Positives = 477/477 (100%), at 1,1-477,477

DNA59606.nc 1 MTSKFILVSFILAALSLSTTFSQLDQQKVLLVSFDGFRWDYLYKVPTPHFHYIMKYGVH

P_AAU12397 1 MTSKFILVSFILAALSLSTTFSQLDQQKVLLVSFDGFRWDYLYKVPTPHFHYIMKYGVH

DNA59606.nc 61 VKQVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNKSFSLDHMNIYDSKFWEA

P_AAU12397 61 VKQVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNKSFSLDHMNIYDSKFWEA

DNA59606.nc 121 TPIWITNQRAGHTSGAAMWPGTDVKIHKRFPPTHMPYNESVSFEDRVAKIVEWFTSKEPI

P_AAU12397 121 TPIWITNQRAGHTSGAAMWPGTDVKIHKRFPPTHMPYNESVSFEDRVAKIVEWFTSKEPI

DNA59606.nc 181 NLGLLYWEDPDDMGHHLGPDSPLMGPVISIDKKLGYLIQMLKKAKLWNTLNLIITSDHG

P_AAU12397 181 NLGLLYWEDPDDMGHHLGPDSPLMGPVISIDKKLGYLIQMLKKAKLWNTLNLIITSDHG

DNA59606.nc 241 MTQCSEERLIELDQYLDKDHYTLIDQSPVAAILPKEGKFDEVYEALTHAHPNLTVYKKED

P_AAU12397 241 MTQCSEERLIELDQYLDKDHYTLIDQSPVAAILPKEGKFDEVYEALTHAHPNLTVYKKED

DNA59606.nc 301 VPERWHYKYNNSRIQPIIAVADEGWHILQNKSDDFLLGNHGYDNALADMPIFLAHGPAFR

P_AAU12397 301 VPERWHYKYNNSRIQPIIAVADEGWHILQNKSDDFLLGNHGYDNALADMPIFLAHGPAFR

DNA59606.nc 361 KNFSKEAMNSTDLYPLLCHLLNITAMPHNGSFNVQDLLNSAMPRVVPYTQSTILLPGSV

P_AAU12397 361 KNFSKEAMNSTDLYPLLCHLLNITAMPHNGSFNVQDLLNSAMPRVVPYTQSTILLPGSV

DNA59606.nc 421 KPAEYDQEGSYPYFIGVSLGSIIVIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA

P_AAU12397 421 KPAEYDQEGSYPYFIGVSLGSIIVIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA

>3 P_AAY66716 Membrane-bound protein PRO1107 - Homo sapiens. (477 aa) [1 seg]
Score = 2561 (991 bits), Expect = 0.0
Identities = 477/477 (100%), Positives = 477/477 (100%), at 1,1-477,477

DNA59606.nc 1 MTSKFILVSFILAALSLSTTFSQLDQQKVLLVSFDGFRWDYLYKVPTPHFHYIMKYGVH

P_AAY66716 1 MTSKFILVSFILAALSLSTTFSQLDQQKVLLVSFDGFRWDYLYKVPTPHFHYIMKYGVH

DNA59606.nc 61 VKQVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNKSFSLDHMNIYDSKFWEA

P_AAY66716 61 VKQVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNKSFSLDHMNIYDSKFWEA

DNA59606.nc 121 TPIWITNQRAGHTSGAAMWPGTDVKIHKRFPPTHMPYNESVSFEDRVAKIVEWFTSKEPI

P_AAY66716 121 TPIWITNQRAGHTSGAAMWPGTDVKIHKRFPPTHMPYNESVSFEDRVAKIVEWFTSKEPI

DNA59606.nc 181 NLGLLYWEDPDDMGHHLGPDSPLMGPVISIDKKLGYLIQMLKKAKLWNTLNLIITSDHG

P_AAY66716 181 NLGLLYWEDPDDMGHHLGPDSPLMGPVISIDKKLGYLIQMLKKAKLWNTLNLIITSDHG

DNA59606.nc 241 MTQCSEERLIELDQYLDKDHYTLIDQSPVAAILPKEGKFDEVYEALTHAHPNLTVYKKED

P_AAY66716 241 MTQCSEERLIELDQYLDKDHYTLIDQSPVAAILPKEGKFDEVYEALTHAHPNLTVYKKED

DNA59606.nc 301 VPERWHYKYN SRIQPIIAVADEGWHILQNK SDDFL LGN HGYDNALADMHP IFLA HGP AFR

 P_AAY66716 301 VPERWHYKYN SRIQPIIAVADEGWHILQNK SDDFL LGN HGYDNALADMHP IFLA HGP AFR

 DNA59606.nc 361 KNFSKEAMNSTDLYPLLCHLLNITAMPHNGSF WNQD LNSAMPRV VPY TQSTILLPGSV

 P_AAY66716 361 KNFSKEAMNSTDLYPLLCHLLNITAMPHNGSF WNQD LNSAMPRV VPY TQSTILLPGSV

 DNA59606.nc 421 KPAEYDQEGSYPYFIGVSLGSIIIVIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA

 P_AAY66716 421 KPAEYDQEGSYPYFIGVSLGSIIIVIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA

>4 P_AAB24072 Human PRO1107 protein sequence SEQ ID NO:44 - Homo sapiens. (477 aa) [1 seg]

Score = 2561 (991 bits), Expect = 0.0
 Identities = 477/477 (100%), Positives = 477/477 (100%), at 1,1-477,477

DNA59606.nc 1 MTSKFILVSFILAALSLSTTFSLQLDQQKVLLVSFDGFRWDYLYKVPTPHFHYIMKYGVH

 P_AAB24072 1 MTSKFILVSFILAALSLSTTFSLQLDQQKVLLVSFDGFRWDYLYKVPTPHFHYIMKYGVH

 DNA59606.nc 61 VKQVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNKSFSLDHMNIYDSKFWEA

 P_AAB24072 61 VKQVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNKSFSLDHMNIYDSKFWEA

 DNA59606.nc 121 TPIWITNQRAGHTSGAAMWPGTDVKIHKRFP THYMPYNESVS FEDRVAKI VEWFTSKEPI

 P_AAB24072 121 TPIWITNQRAGHTSGAAMWPGTDVKIHKRFP THYMPYNESVS FEDRVAKI VEWFTSKEPI

 DNA59606.nc 181 NLGLLYWEDPDDMGHHLGPDSPLMGPVIS DIDKKLGYLIQMLKKAKLWNTLNLIITS DHG

 P_AAB24072 181 NLGLLYWEDPDDMGHHLGPDSPLMGPVIS DIDKKLGYLIQMLKKAKLWNTLNLIITS DHG

 DNA59606.nc 241 MTQCSEERLIELDQYLDKDHYTLIDQSPVAA ILPKEGKFDEVYEALTHAHPNLTVYKKED

 P_AAB24072 241 MTQCSEERLIELDQYLDKDHYTLIDQSPVAA ILPKEGKFDEVYEALTHAHPNLTVYKKED

 DNA59606.nc 301 VPERWHYKYN SRIQPIIAVADEGWHILQNK SDDFL LGN HGYDNALADMHP IFLA HGP AFR

 P_AAB24072 301 VPERWHYKYN SRIQPIIAVADEGWHILQNK SDDFL LGN HGYDNALADMHP IFLA HGP AFR

 DNA59606.nc 361 KNFSKEAMNSTDLYPLLCHLLNITAMPHNGSF WNQD LNSAMPRV VPY TQSTILLPGSV

 P_AAB24072 361 KNFSKEAMNSTDLYPLLCHLLNITAMPHNGSF WNQD LNSAMPRV VPY TQSTILLPGSV

 DNA59606.nc 421 KPAEYDQEGSYPYFIGVSLGSIIIVIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA

 P_AAB24072 421 KPAEYDQEGSYPYFIGVSLGSIIIVIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA

>5 P_AAE05491 Human phosphodiesterase-1 (HPDE-1) - Homo sapiens. (477 aa) [1 seg]

Score = 2553 (988 bits), Expect = 0.0
 Identities = 475/477 (99%), Positives = 476/477 (99%), at 1,1-477,477

DNA59606.nc 1 MTSKFILVSFILAALSLSTTFSLQLDQQKVLLVSFDGFRWDYLYKVPTPHFHYIMKYGVH

P_AAE05491 1 MTSKFILVSFILAALSLSTTFSLQPDQQKVLLVSFDGFRWDYLYKVPTPHFHYIMKYGVH

DNA59606.nc 61 VKQVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNSFSLDHMNIYDSKFWEA

P_AAE05491 61 VKQVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNSFSLDHMNIYDSKFWEA

DNA59606.nc 121 TPIWITNQRAGHTSGAAMWPGTDVKIHKRFPYHMPYNESVSFEDRVAKIVEWFTSKEPI

P_AAE05491 121 TPIWITNQRAGHTSGAAMWPGTDVKIHKRFPYHMPYNESVSFEDRVAKIIEWFTSKEPI

DNA59606.nc 181 NLGLLYWEDPDDMGHHLGPDSPLMGPVISDIDKKLGYLIQMLKKAKLWNTLNLIITSDHG

P_AAE05491 181 NLGLLYWEDPDDMGHHLGPDSPLMGPVISDIDKKLGYLIQMLKKAKLWNTLNLIITSDHG

DNA59606.nc 241 MTQCSEERLIELDQYLDKDHYTLIDQSPVAAILPKEGKFDEVYEALTHAHPNLTVYKKED

P_AAE05491 241 MTQCSEERLIELDQYLDKDHYTLIDQSPVAAILPKEGKFDEVYEALTHAHPNLTVYKKED

DNA59606.nc 301 VPERWHYKYNNSRIQPIIAVADEGWHILQNKSDDFLLGNHGYDNALADMHPIFLAHGPAGR

P_AAE05491 301 VPERWHYKYNNSRIQPIIAVADEGWHILQNKSDDFLLGNHGYDNALADMHPIFLAHGPAGR

DNA59606.nc 361 KNFSKEAMNSTDLYPLLCHLLNITAMPHNGSFWNVQDLLNSAMPRVVPYTQSTILLPGSV

P_AAE05491 361 KNFSKEAMNSTDLYPLLCHLLNITAMPHNGSFWNVQDLLNSAMPRVVPYTQSTILLPGSV

DNA59606.nc 421 KPAEYDQEGSYPYFIGVSLGSIIVIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA

P_AAE05491 421 KPAEYDQEGSYPYFIGVSLGSIIVIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA

>6 CAB56566.1 dJ8B1.3 (similar to PLASMA-CELL MEMBRANE GLYCOPROTEIN PC-1) - Homo sapiens (477 aa) [1 seg]
Score = 2551 (987 bits), Expect = 0.0
Identities = 474/477 (99%), Positives = 476/477 (99%), at 1,1-477,477.

DNA59606.nc 1 MTSKFILVSFILAALSLSTTFSLQLDQQKVLLVSFDGFRWDYLYKVPTPHFHYIMKYGVH

CAB56566.1 1 MTSKFLLVSFILAALSLSTTFSLQPDQQKVLLVSFDGFRWDYLYKVPTPHFHYIMKYGVH

DNA59606.nc 61 VKQVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNSFSLDHMNIYDSKFWEA

CAB56566.1 61 VKQVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNSFSLDHMNIYDSKFWEA

DNA59606.nc 121 TPIWITNQRAGHTSGAAMWPGTDVKIHKRFPYHMPYNESVSFEDRVAKIVEWFTSKEPI

CAB56566.1 121 TPIWITNQRAGHTSGAAMWPGTDVKIHKRFPYHMPYNESVSFEDRVAKIIEWFTSKEPI

DNA59606.nc 181 NLGLLYWEDPDDMGHHLGPDSPLMGPVISDIDKKLGYLIQMLKKAKLWNTLNLIITSDHG

CAB56566.1 181 NLGLLYWEDPDDMGHHLGPDSPLMGPVISDIDKKLGYLIQMLKKAKLWNTLNLIITSDHG

DNA59606.nc 241 MTQCSEERLIELDQYLDKDHYTLIDQSPVAAILPKEGKFDEVYEALTHAHPNLTVYKKED

CAB56566.1 241 MTQCSEERLIELDQYLDKDHYTLIDQSPVAAILPKEGKFDEVYEALTHAHPNLTVYKKED

DNA59606.nc 301 VPERWHYKYNNSRIQPIIAVADEGWHILQNKSDDFLLGNHGYDNALADMHPIFLAHGPAGR

CAB56566.1 301 VPERWHYKYN SRIQPIIAVADEGWHILQNK SDDFLLGNHGYDNALADMHP IFLAHGPAFR

DNA59606.nc 361 KNFSKEAMNSTDLYPLLCHLLNITAMPHNGSFWNVQDLLNSAMPRVVPYTQSTILLPGSV

CAB56566.1 361 KNFSKEAMNSTDLYPLLCHLLNITAMPHNGSFWNVQDLLNSAMPRVVPYTQSTILLPGSV

DNA59606.nc 421 KPAEYDQEGSYPYFIGVSLGSIIIVIVFFVIFIKHLIHSQI PALQDMHAEIAQPLLQA

CAB56566.1 421 KPAEYDQEGSYPYFIGVSLGSIIIVIVFFVIFIKHLIHSQI PALQDMHAEIAQPLLQA

>7 NP_067547.1 ectonucleotide pyrophosphatase/phosphodiesterase 5 (putative function) - Homo sapiens (477 aa) [1 seg]
Score = 2551 (987 bits), Expect = 0.0
Identities = 474/477 (99%), Positives = 476/477 (99%), at 1,1-477,477

DNA59606.nc 1 MTSKFILVSFILAALSLSTTFS LQDQQKVLLVSFDGFRWDYLYKVPTPHFHYIMKYGVH

NP_067547.1 1 MTSKFLLVSFILAALSLSTTFS LQPDQQKVLLVSFDGFRWDYLYKVPTPHFHYIMKYGVH

DNA59606.nc 61 VKQVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNKSFSLDHMNIYDSKFWEA

NP_067547.1 61 VKQVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNKSFSLDHMNIYDSKFWEA

DNA59606.nc 121 TPIWITNQRAGHTSGAAMWPGTDVKIHKRFPTHYMPYNESVSFEDRVAKIIEWFTSKEPI

NP_067547.1 121 TPIWITNQRAGHTSGAAMWPGTDVKIHKRFPTHYMPYNESVSFEDRVAKIIEWFTSKEPI

DNA59606.nc 181 NLGLLYWEDPDDMGHHLGPDSPLMGPVISDIDKKLGYLIQMLKKAKLWNTLNLIITSDHG

NP_067547.1 181 NLGLLYWEDPDDMGHHLGPDSPLMGPVISDIDKKLGYLIQMLKKAKLWNTLNLIITSDHG

DNA59606.nc 241 MTQCSEERLIELDQYLDKDH YTLIDQSPVAA ILPKEGKFDEVYEALTHAHPNLTVYKKED

NP_067547.1 241 MTQCSEERLIELDQYLDKDH YTLIDQSPVAA ILPKEGKFDEVYEALTHAHPNLTVYKKED

DNA59606.nc 301 VPERWHYKYN SRIQPIIAVADEGWHILQNK SDDFLLGNHGYDNALADMHP IFLAHGPAFR

NP_067547.1 301 VPERWHYKYN SRIQPIIAVADEGWHILQNK SDDFLLGNHGYDNALADMHP IFLAHGPAFR

DNA59606.nc 361 KNFSKEAMNSTDLYPLLCHLLNITAMPHNGSFWNVQDLLNSAMPRVVPYTQSTILLPGSV

NP_067547.1 361 KNFSKEAMNSTDLYPLLCHLLNITAMPHNGSFWNVQDLLNSAMPRVVPYTQSTILLPGSV

DNA59606.nc 421 KPAEYDQEGSYPYFIGVSLGSIIIVIVFFVIFIKHLIHSQI PALQDMHAEIAQPLLQA

NP_067547.1 421 KPAEYDQEGSYPYFIGVSLGSIIIVIVFFVIFIKHLIHSQI PALQDMHAEIAQPLLQA

>8 A59391 probable phosphodiesterase I (EC 3.1.4.1) / nucleotide pyrophosphatase (EC 3.6.1.9) 5 - human (477 aa) [1 seg]
Score = 2551 (987 bits), Expect = 0.0
Identities = 474/477 (99%), Positives = 476/477 (99%), at 1,1-477,477

DNA59606.nc 1 MTSKFILVSFILAALSLSTTFS LQDQQKVLLVSFDGFRWDYLYKVPTPHFHYIMKYGVH

A59391 1 MTSKFLLVSFILAALSLSTTFS LQPDQQKVLLVSFDGFRWDYLYKVPTPHFHYIMKYGVH

DNA59606.nc 61 VKQVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNKSFSLDHMNIYDSKFWEA

A59391 61 VKQVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNSFSLDHMNIYDSKFWEAA

DNA59606.nc 121 TPIWITNQRAGHTSGAACWPGTDVKIHKRFPYHMPYNESVSFEDRVAKIVEWFTSKEPI

A59391 121 TPIWITNQRAGHTSGAACWPGTDVKIHKRFPYHMPYNESVSFEDRVAKIEWFTSKEPI

DNA59606.nc 181 NLGLLYWEDPDDMGHHLGPDSPLMGPVISIDKKLGYLIQMLKKAKLWNTLNLIITSDHG

A59391 181 NLGLLYWEDPDDMGHHLGPDSPLMGPVISIDKKLGYLIQMLKKAKLWNTLNLIITSDHG

DNA59606.nc 241 MTQCSEERLIELDQYLDKDHYTLIDQSPVAAILPKEGKFDEVYEALTHAHPNLTVYKKED

A59391 241 MTQCSEERLIELDQYLDKDHYTLIDQSPVAAILPKEGKFDEVYEALTHAHPNLTVYKKED

DNA59606.nc 301 VPERWHYKYNNSRQPIIAVADEGWHILQNKSDDFLLGNHGYDNALADMHPIFLAHGPFR

A59391 301 VPERWHYKYNNSRQPIIAVADEGWHILQNKSDDFLLGNHGYDNALADMHPIFLAHGPFR

DNA59606.nc 361 KNFSKEAMNSTDLYPLLCHLLNITAMPHNGSFNVQDLLNSAMPRVVPYTQSTILLPGSV

A59391 361 KNFSKEAMNSTDLYPLLCHLLNITAMPHNGSFNVQDLLNSAMPRVVPYTQSTILLPGSV

DNA59606.nc 421 KPAEYDQEGSYPYFIGVSLGSIIVIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA

A59391 421 KPAEYDQEGSYPYFIGVSLGSIIVIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA

>9 P_AAM23765 Human EST encoded protein SEQ ID NO: 1290 - Homo sapiens. (452 aa)
[1 seg]
Score = 2403 (930 bits), Expect = 0.0
Identities = 446/451 (98%), Positives = 447/451 (98%), at 1,1-451,451

DNA59606.nc 1 MTSKFILVSFILAALSLSTTFSLOLDQQKVLLVSFDGFRWDYLYKVPTPHFHYIMKYGVH

P_AAM23765 1 MTSKFILVSFILAALSLSTTFSLOPDQQKVLLVSFDGFRWDYLYKVPTPHFHYIMKYGVH

DNA59606.nc 61 VKQVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNSFSLDHMNIYDSKFWEAA

P_AAM23765 61 VKQVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNSFSLDHMNIYDSKFWEAA

DNA59606.nc 121 TPIWITNQRAGHTSGAACWPGTDVKIHKRFPYHMPYNESVSFEDRVAKIVEWFTSKEPI

P_AAM23765 121 TPIWITNQRAGHTSGAACWPGTDVKIHKRFPYHMPYNESVSFEDRVAKIEWFTSKEPI

DNA59606.nc 181 NLGLLYWEDPDDMGHHLGPDSPLMGPVISIDKKLGYLIQMLKKAKLWNTLNLIITSDHG

P_AAM23765 181 NLGLLYWEDPDDMGHHLGPDSPLMGPVISIDKKLGYLIQMLKKAKLWNTLNLIITSDHG

DNA59606.nc 241 MTQCSEERLIELDQYLDKDHYTLIDQSPVAAILPKEGKFDEVYEALTHAHPNLTVYKKED

P_AAM23765 241 MTQCSEERLIELDQYLDKDHYTLIDQSPVAAILPKEGKFDEVYEALTHAHPNLTVYKKED

DNA59606.nc 301 VPERWHYKYNNSRQPIIAVADEGWHILQNKSDDFLLGNHGYDNALADMHPIFLAHGPFR

P_AAM23765 301 VPERWHYKYNNSRQPIIAVADEGWHILQNKSDDFLLGNHGYHNAADMHPIFLAHGPFR

DNA59606.nc 361 KNFSKEAMNSTDLYPLLCHLLNITAMPHNGSFNVQDLLNSAMPRVVPYTQSTILLPGSV

P_AAM23765 361 KNFSKEAMNSTDLYPLLCHLLNITAMPHNGSFVNQDLLNSAMPRVVPTQSTILLPGSV
DNA59606.nc 421 KPAEYDQEGSYPYFIGVSLGSIIIVIVFFVIF

*
P_AAM23765 421 KPAEYDQEGSYPYFIGVSLGSIIIVIVFFCNF